

10 30 50
 GCACGAGCTGCCTCCCGCAGGCGCCACCTGTGTCCCCAGCGCCGCTCCACCCAGCAGGC
 70 90 110
 CTGAGCCCCTCTCTGCTGCCAGACACCCCTGCTGCCCACTCTCCTGCTGCTCGGGTTCT
 130 150 170
 GAGGCACAGCTTGTACACCGAGGCGGATTCTTTTCTTTTCTTTTCTTTTCTTTCTGGCCC
 190 210 230
 ACAGCCGCAGCAATGGCGCTGAGTTCCTCTGCTGGAGTTCATCCTGCTAGCTGGGTTCCC
 250 270 290
 GAGCTGCCGGTCTGAGCCTGAGGCATGGAGCCTCCTGGAGACTGGGGGCCTCCTCCCTGG
 M E P P G D W G P P P W
 310 330 350
 AGATCCACCCCAAAACCGACGTCTTGAGGCTGGTGCTGTATCTCACCTTCCTGGGAGCC
 R S T P K T D V L R L V L Y L T F L G A
 370 390 410
 CCCTGCTACGCCCCAGCTCTGCCGTCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAG
 P C Y A P A L P S C K E D E Y P V G S E
 430 450 470
 TGCTGCCCAAGTGCAGTCCAGGTTATCGTGTGAAGGAGGCCTGCGGGGAGCTGACGGGC
 C C P K C S P G Y R V K E A C G E L T G
 490 510 530
 ACAGTGTGTGAACCCTGCCCTCCAGGCACCTACATTGCCACCTCAATGGCCTAAGCAAG
 T V C E P C P P G T Y I A H L N G L S K
 550 570 590
 TGTCTGCAGTGCCAAATGTGTGACCCAGCCATGGGCCTGCGCGGAGCCGGAAGTGTCTCC
 C L Q C Q M C D P A M G L R A S R N C S
 610 630 650
 AGGACAGAGAACGCCGTGTGTGGTTGCAGCCCAGGCCACTTCTGCATCGTCCAGGACGGG
 R T E N A V C G C S P G H F C I V Q D G
 670 690 710
 GACCACTGCGCCGCGTGCCGCGCTTACGCCACCTCCAGCCCGGGCCAGAGGGTGCAGAAG
 D H C A A C R A Y A T S S P G Q R V Q K
 730 750 770
 GGAGGCACCGAGAGTCAGGACACCCTGTGTGCAAGTGTGCCCCCGGGACCTTCTCTCCC
 G G T E S Q D T L C Q N C P P G T F S P
 790 810 830
 AATGGGACCCTGGAGGAATGTCAGCACCAGACCAAGTGCAGCTGGCTGGTGACGAAGGCC
 N G T L E E C Q H Q T K C S W L V T K A
 850 870 890
 GGAGCTGGGACCAGCAGCTCCCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATC
 G A G T S S S H W V W W F L S G S L V I

FIG. 1A

```

      910              930              950
GTCATTGTTTGCTCCACAGTTGGCCTAATCATATGTGTGAAAAGAAGAAAGCCAAGGGGT
V  I  V  C  S  T  V  G  L  I  I  C  V  K  R  R  K  P  R  G
      970              990              1010
GATGTAGTCAAGGTGATCGTCTCCGTCCAGCGGAAAAGACAGGAGGCAGAAAGGTGAGGCC
D  V  V  K  V  I  V  S  V  Q  R  K  R  Q  E  A  E  G  E  A
      1030             1050             1070
ACAGTCATTGAGGCCCTGCAGGCCCTCCGGACGTCAACACGGTGGCCGTGGAGGAGACA
T  V  I  E  A  L  Q  A  P  P  D  V  T  T  V  A  V  E  E  T
      1090             1110             1130
ATACCCTCATTACGGGGAGGAGCCCAAACCACTGACCCACAGACTCTGCACCCCGACGC
I  P  S  F  T  G  R  S  P  N  H  *
      1150             1170             1190
CAGAGATACCTGGAGCGACGGCTGAATGAAAGAGGCTGTCCACCTGGCGGAACCAACCGGA
      1210             1230             1250
GCCCCGAGGCTTGGGGGCTCCACCCTGGACTGGCTTCCGTCTCCTCCAGTGGAGGGAGAG
      1270             1290             1310
GTGGCGCCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCCATGGGCCAGTGAG
      1330             1350             1370
GGCCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCCTGAGGAGGAGCGCCA
      1390             1410             1430
GTTGCCCCTCGCTCACAGACCACACACCCAGCCCTCCTGGGCCAACCCAGAGGGCCTTCA
      1450             1470             1490
GACCCAGCTGTGTGCGCGTCTGACTCTTGTGGCCTCAGCAGGACAGGCCCGGGCACTG
      1510             1530             1550
CCTCACAGCCAAGGCTGGACTGGGTTGGCTGCAGTGTGGTGTGTTAGTGGATACCACATCG
      1570             1590             1610
GAAGTGATTTTCTAAATTGGATTTGAATTCGGCTCCTGTTTTCTATTTGTCATGAAACAG
      1630             1650             1670
TGATTTTGGGGAGATGCTGTGGGAGGATGTAAATATCTTGTTTCTCCTCAAAAAAAAAA
      1690
AAAAAAAAAAAAAAAAAAAAAAAAA

```

FIG.1B

1	MEPPGDWGPPPWRSTPKTDVLRVLVLYLTFLGAPCYAPALPSCKEDEYVPV	50
1MVSLPRLCALWGCLLTAVHLGQCVTCSDKQYLHD	34
51	SECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCD	100
35	GQCCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQHRHCE	84
101	PAMGLRASRNCSTENAVCGCSPGHFCIVQGDGHCAACRAYATSSPGQRV	150
85	PNQGLRVKKEGTAESDTVCTCKEGQHCTSKD...CEACAQHTPCIPGFGV	131
151	QKGGTESQDTLCQNCPPGTFSPNGTL.EECQHQT KC.SWLVT KAGAGTSS	198
132	MEMATETTTDTVCHPCPCGFFSNQSSLFEKCYPNTSCEDKNLEVLQKGTSQ	181
199	SH.....WWWFLSGSLVIVIVCSTVGLIICVKR..RKPRGDVVKVIV	239
182	TNVICGLKSRMRALLVIPVVMGILITIFGVFLYIKKVVKPKDNEMLPPA	231
240	SVQRKRQEAEG.....EATVIEALQAPPDVTTVAVEETIPSFTGRSPNH	283
232	ARRODPQEMEDYPGHNTAAPVOETLHGCPVTQEDGKESRISVQERQVTD	281

FIG. 2

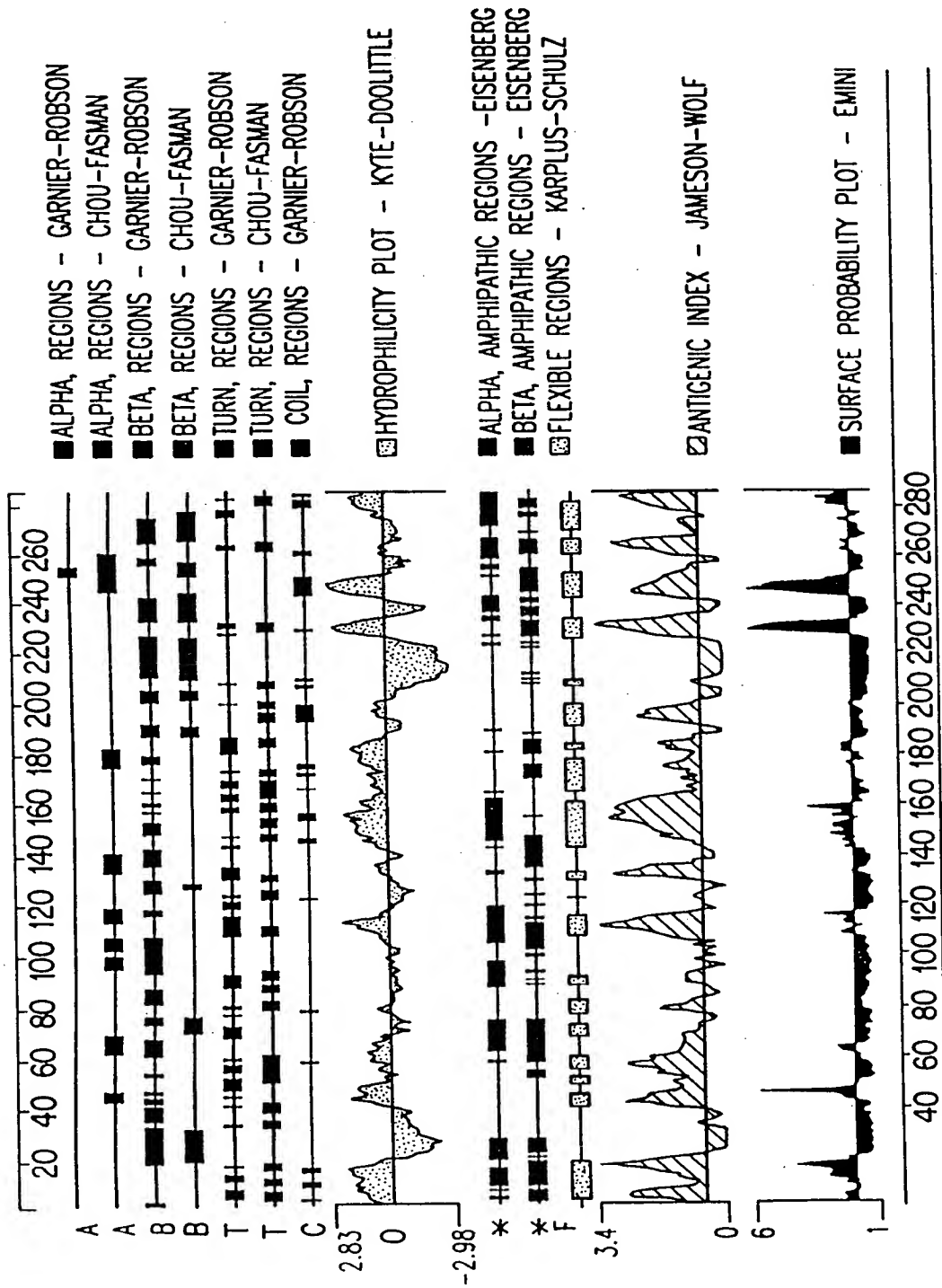


FIG. 3

```

      10              30              50
CCCCCTTCTACAGGAAACCCGGAGTGGACTGGAACGGTGCAGGGGGAGAACTCGCCCCTC
      70              90              110
CCATCGGGGCGCCTCCTTCATACCGGCCCTTCCCCTCGGCTTTGCCTGGACAGCTCCTGCC
      130             150             170
TCAGGCAGCGCCACCTGTGTCGCCCAGCGCCGCTCCACCCAGCAGGCCTGAGCCCCTCTC
      190             210             230
TGCTGCCAGACACCCCCTGCTGCCCACTACTCCTGCTGCTCGGGTTCTGAGGCACAGCTT
      250             270             290
GTCACACCGAGGCGGATTCTCTTTCTCTTTCTCTTTCTCTTCTGGCCCACAGCCGCAGCA
      310             330             350
ATGGCGCTGAGTTCCTCTGCTGGAGTTCATCCTGCTAGCTGGGTTCCCGAGCTGCCGGTC
      370             390             410
TGAGCCTGAGTCATGGAGCCTCCTGGAGACTGGGGGCCTCCTCCCTGGAGATCCACCCCC
      M E P P G D W G P P P W R S T P
      430             450             470
AGAACCGACGTCTTGAGGCTGGTGTGTATCTCACCTTCCTGGGAGCCCCCTGCTACGCC
      R T D V L R L V L Y L T F L G A P C Y A
      490             510             530
CCAGCTCTGCCGTCTCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGCTGCCCAAG
      P A L P S C K E D E Y P V G S E C C P K
      550             570             590
TGCAGTCCAGGTTATCGTGTGAAGGAGGCCCTGCGGGGAGCTGACGGGCACAGTGTGTGAA
      C S P G Y R V K E A C G E L T G T V C E
      610             630             650
CCCTGCCCTCCAGGCACCTACATTGCCACCTCAATGGCCTAAGCAAGTGTCTGCAGTGC
      P C P P G T Y I A H L N G L S K C L Q C
      670             690             710
CAAATGTGTGACCCAGATATTGGTTCCCCCTGTGACCTCAGGGGAAGAGGTACCTGGAG
      Q M C D P D I G S P C D L R G R G H L E
      730             750             770
GCTGGTGCCACCTGAGTCCAGGCAGACAGAAAGGGGAACCAGACCCAGAGGTGGCCTTT
      A G A H L S P G R Q K G E P D P E V A F
      790             810             830
GAGTCACTGAGCGCAGAGCCTGTCCATGCGGCCAACGGCTCTGTCCCCTTGGAGCCTCAT
      E S L S A E P V H A A N G S V P L E P H
      850             870             890
GCCAGGCTCAGCATGGCCAGTGCTCCCTGCGGCCAGGCAGGACTGCACCTGCGGGACAGG
      A R L S M A S A P C G Q A G L H L R D R
      910             930             950
GCTGACGGCACACCTGGGGGCAGGGCCTGAGCCTACAGGGAGGCACAGGGCAGGTGGGCT
      A D G T P G G R A *

```

FIG.4A

970	990	1010
AGCCATGAACAGAAGAGGAAGCTGGAGTGCTTTGGGGGTT	CATGCATGTAGGCTGGGATT	
1030	1050	1070
TGGGGCTCACACCTCAACCTGCATGCCAGTTCCATGCCCTCCCCTCTTGTGAAAGCAC		
1090	1110	1130
CTGTCTACTTGGGCTGAGGATGTGGGGGCACAGGTGGCAGGTGAGGCTGCCCTCAGGAGG		
1150	1170	1190
GGCCCAGGCCAGCTTGTACCCACCTCCACCACTGACCTGAAGAAGTGGGGCTCTCACCC		
1210	1230	1250
TACCTGCCTCTGCCATTGGAATGGCCTGGTTTGCACAGATGGGAAACCCGTTTGAGGGGT		
1270	1290	1310
GGGTGTCTGGGTGGGCACGTGGGGCGAGGACCTGCCTGAGGGACCCTGCCCTGGAAGTGA		
1330	1350	1370
CAGTGCAAGCTCGGCGTCTGCCATCTGGGCAGAAGGCTGGTTTCTCCCATCAACGAAG		
1390	1410	1430
CCCTCCAGGACCTTCCTGCAAGCCCTCGTCCCACACGCAGCTCTGCCGTCCCTTGGTGT		
1450	1470	1490
CCCTCCCGGCCTCAGGTCCTCCATGCTGGGTACCTCTGGGCACCTCGTTTGGCTGAGCCA		
1510	1530	1550
GGGGTTCAGCCTGGCAGGGCGCCCTGGCAGCAGTCCTTGGCCTGTGGATGCTGTCCTGGC		
1570	1590	1610
CTGTGGATGGTGTCCCGCCCTCCACGTACCCCTCTCACCCCTCCTCTTGGACTCCAGCC		
1630	1650	1670
ATGGGCCTGCGCGGAGCCGGAAGTCTCCAGGACAGAGAACGCCGTGTGTGGCTGCAGC		
1690	1710	1730
CCAGGCCACTTCTGCATCGTCCAGGACGGGGACCACTGCGCCGCGTGCCGCGCTTACGCC		
1750	1770	1790
ACCTCCAGCCCGGGCCAGAGGGTGCAGAAGGGAGGCACCGAGAGTCAGGACACCCTGTGT		
1810	1830	1850
CAGAACTGCCCCCGGGGACCTTCTCTCCAATGGGACCCTGGAGGAATGTCAGCACCAG		
1870	1890	1910
ACCAATTGGCCTAATCATATGTGTGAAAAGAAGAAAGCCAAGGGGTGAGCACACGGTGGC		
1930	1950	1970
CCCATCAGGGTTCATGTCCCCAGCCGTACCTCTTGGAGCTCTGTACCCCAAGCCTGGG		
1990	2010	2030
AGGTGGCCCCAGAGCTTTTCCAGGATCCGCGGCTCCTCCAGGGCAGCCACTGCAGGCTG		
2050	2070	2090
GGGCAGGTGTATGTAGTCAAGGTGATCGTCTCCGTCCAGCGGTAAAAGACAGGAGGCAGA		
2110	2130	2150
AGGTGAGGCCACAGTCATTGAGCCCTGCAGGCCCTCCGGACGTCACCACGGTGGCCGTG		
2170	2190	2210
GAGGAGACAATACCCTCATTCACGGGGAGGAGCCCAAACCACTGACCCACAGACTCTGCA		

FIG.4B

2230	2250	2270
CCCCGACGCCAGAGATACCTGGAGAGACGGCTGCTGATAGAGGCTGTCCACCTGGCGAAA		
2290	2310	2330
CCACCGGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGTTTCCGTCTCCTCCAGTGG		
2350	2370	2390
AGGGAGAGGTGGTGCCCCTGCTGGTGGTAGAGCTGGGGACGCCACGTGCCATTCCCATTGG		
2410	2430	2450
TTCAGTGAGGGGCTGGTGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCCTGAGG		
2470	2490	2510
AGGAGCCCCAGTTGCCCTCGCTCACAGACCACACCCAGCCCTCCTGGGCCAACCCAG		
2530	2550	2570
AGGCCCTTCAGACCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCAGGACAGGC		
2590	2610	2630
CCCGGGCACTGCCTCACAGCCAAGGCTGGAATGGGTTGGCTGCAGTGTGGTGTGTTAGTGG		
2650	2670	2690
ATACCACATCGGAAGTGATTTTCTAAAAATTGGATTTGAATTCGGAAAAAAA		

FIG.4C

1	MEPPGDWGPPPWRSTPRTDVLRRLVLYLTFLGAPCYAPALPSCKEDEY..P	48
	. .: ::: . :... . :. . : :.:.. : .	
1	MAPVAVWAALAVGLELWAAHALPAQVAF..TPYAPEPGSTCRLREYYDQ	48
49	VGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQM	98
	.: . :. .. :. : ..: :.. .	
49	TAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGS	98
99	..CDPDIGSPCDLRGRGHL.....EAGAHLSRGRQKGEPDPE	133
	:..... :..... :. : :.. . . : :	
99	RCSSDQVETQACTREQNRICRPGWYCALSKQEGCRLCAPLRKCRPGFG	148
134	VA.....FESLSAEPVHAANGS	150
	:.: .: .:.	
149	VARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDA	198
151	VPLEPHARLSMASAPC..GQAGLHLRDRADGTPGGRA.....	185
	. . . : .:.:..: :....	
199	VCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPS	248

FIG.5

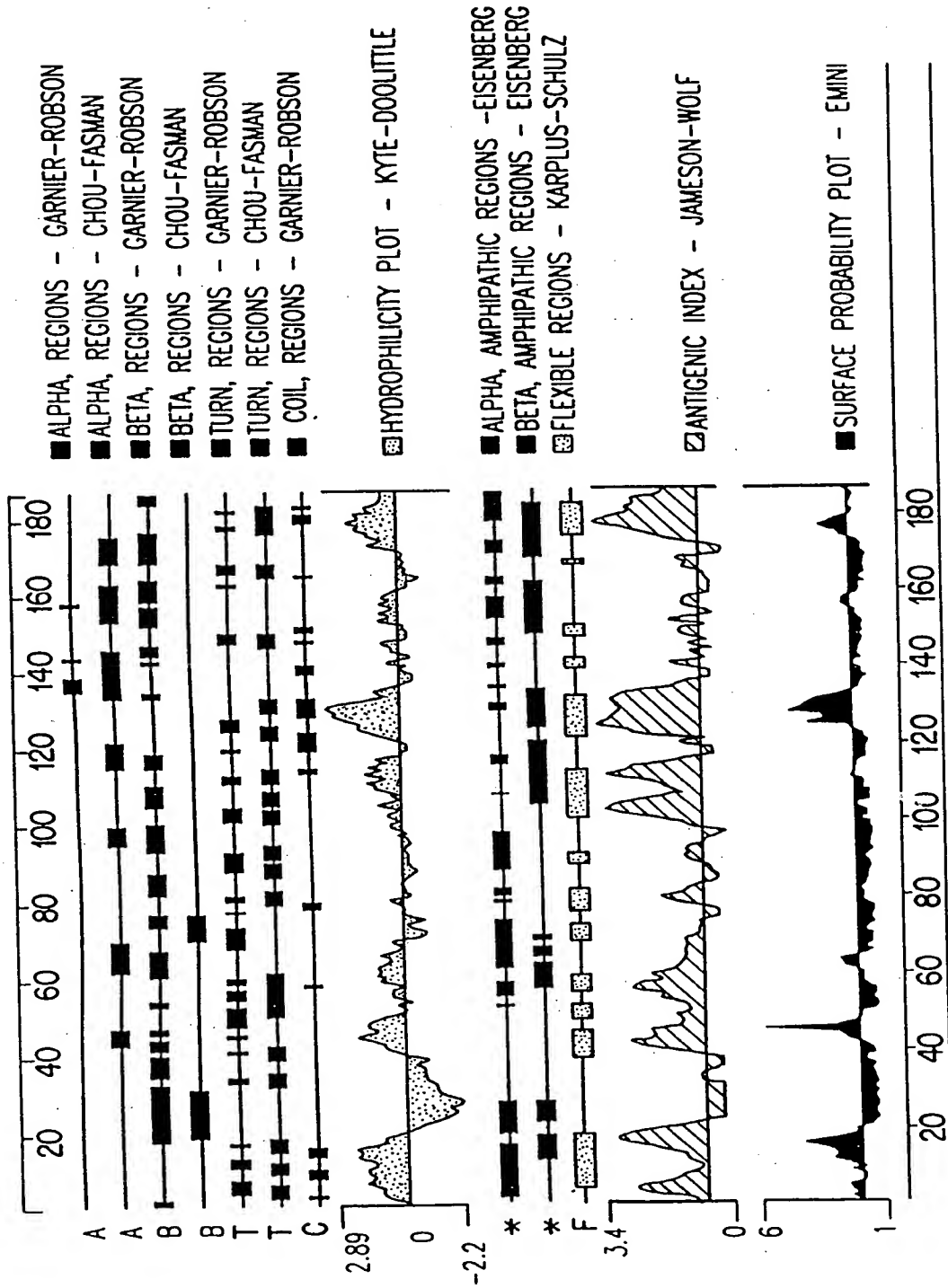


FIG. 6

```

      10              30              50
AAAGCTCGGGCTCCACCGGGGACGACCGCTCCTAGAACTGAGTGGTATCCCCCGGGCCT
      70              90              110
GCAGGAATTCCAACCTGCCTGAAGGGACCCTGCCCTGGAAGTACAGTGAAGCTCGGCG
      130             150             170
TCCTGCCCATCTGGGAAGAAGGCTGGTTTCTCCCATCAACGAAGCCCTCCAGGACCTTC
      190             210             230
CTGCAAGCCCTCGTCCCACACGCAGCTCTGCCGTCCCTTGGTGTCCCTCCCGGCCTCAGG
      250             270             290
TCCTCCATGCTGGGTACCTCTGGGCACCTCGTTTGGCTGAGCCAGGGGTTACAGCTGGCA
      M L G T S G H L V W L S Q G F S L A
      310             330             350
GGGCGCCCTGGCAGCAGTCCTTGGCCTGTGGATGCTGTCTGGCCTGTGGATGGTGTCCC
      G R P G S S P W P V D A V L A C G W C P
      370             390             410
GGCCTCCACGTACCCCTCTCAGCCCTCCTCTTGGACTCCAGCCATGGGCCTGCGCGCG
      G L H V P P L S P S S W T P A M G L R A
      430             450             470
AGCCGGAAGTGTCTCCAGGACAGAGAACGCCGTGTGTGGCTGCAGCCAGGCCACTTCTGC
      S R N C S R T E N A V C G C S P G H F C
      490             510             530
ATCGTCCAGGACGGGGACCACTGCGCCGCGTGCCGCGCTTACGCCACCTCCAGCCCGGGC
      I V Q D G D H C A A C R A Y A T S S P G
      550             570             590
CAGAGGGTGCAGAAGGGAGGCACCGAGAGTCAGGACACCCTGTGTCAGAACTGCCCCCGG
      Q R V Q K G G T E S Q D T L C Q N C P R
      610             630             650
GGACCTTCTCTCCCAATGGGACCCTGGAGGAATGTCAGCACCAAGTAAGTGAACC
      G P S L P M G P W R N V S T R P S K *
      670             690             710
CGGGGGAGGCCAGCTCTGTGCCCTGGGGAGGGGGCTCCACGTTGCTTCCCTGGGAGATGA
      730             750             770
CCGTCTTCTCCAGCAGAAAGGTTGAAGGTCCACCTGAGCGGCACCCTGGTCACATGCC
      790             810             830
TGCGTCCAGGAGAGCTGCAGGGTGAAGCCTGTGTGCCCCAGATAACCCCTTCCATGGGCC
      850             870             890
CAGACAAAGCCTCATCAGATCTGAGCTTCTGGAGGCTCAGGATGGGCCTTCCAGAAGC
      910             930             950
AGGCCAGAGGGAGGCTGCCTCCAGATCCCCTGTCCCCTGGGGCTGTGGGTGTCCCTGAA
      970             990             1010
TGTCAGGGCCATGGGAGGGCCCTGGGCTTCAGGGGTTGGGGAAAGTGAACACTCTGCTC

```

FIG. 7A

1030	1050	1070
TTTGTCCACCTTCGGGAGGACAACCTTCAAATGCTGACCCTGGGCCCCTAACTGACCTGA		
1090	1110	1130
GACTTCAGAGCTTCTTGGGAGGAGCTGGGGTCCCCAGCGGAGCCTGGGATGGAGCAGGG		
1150	1170	1190
ATGGCTGCCCCAGGGAGGGGGCGGTGGGGCCTTCCATCCTGCTCTGCCCTCCTCGTCCTC		
1210	1230	1250
TGGCCCCAGCTCAGTCCTGTCCATCTCCAGCTCTAACCATTGTGGCCCGACACTGGCTC		
1270	1290	1310
TCCCTCTACCTTCTGTCCTTGTCTGACACTGGTCTCCCGTGCTCTGGGGTCTCTGCACTG		
1330	1350	1370
ATGGCTGCCTCCCGCTTCTCTCCCCTCTCCCTCTGCCGTCTGTCTCCTGTGGCCAGTCT		
1390	1410	1430
CTCCTTGTTTCTTCTCTCCTCCTTCTCTCCACCTCCCCATAGCCGAGCTTGAAAA		
1450	1470	1490
GTCAGACAGACCTCTGAGGTCTCATCTGGAGCTGCCACCAGCCCAGCCTCCCTGGGACC		
1510	1530	1550
TGTCTTCACTGCCTGGGGCCCTGGGAGCCAGGGAGGCTCCCTGAGGCTGAGTGAACACTG		
1570	1590	1610
GGCGCTGCACCTGCCTCTCCACGTCTCGGCCCACTCCCGCAGGTGCAGCTGGCTGGT		
1630	1650	1670
GACGAAGCCCGGAGCTGGGACCAGCAGCTCCCACTGGGTATGGTGGTTTCTCTCAGGGAG		
1690	1710	1730
CCTCGTCATCGTCATTGTTTGCTCCACAGTTGGCCTAATCATATGTGTGAAAAGAAGAAA		
1750	1770	1790
GCCAAGGGGTGATGTAGTCAAGGTGATCGTCTCCGTCCAGGTATTGATCCTCCTCCCCCT		
1810	1830	1850
CTCCCTCCCCCTCCACCTTCCACCTCCCCTCTCCCCGCTGGGGCTGGTGTTTCTGGTG		
1870	1890	1910
TACATGGTGGGGGCTCCAGTTCTCTGAGGGTCTGAGTCTTTCAAGTACAGCCACGGTA		
1930	1950	1970
GCTCAGGAAAGAACCCACCCCCTCAAAGTCAAAGCAGTAAAATGAACCCGAGAACCTGGA		
1990	2010	2030
GTCCCAGGGGGGCTGAGCAGGCAGGGTCTCCACGATTCTGTGTGCTCACAGCGGGAAAAAG		
2050	2070	2090
ACAGGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCTCCGGACGTCAC		
2110	2130	2150
CACGGTGGCCGTGGAGGAGACAATACCCTCATTACGGGGGAGGAGCCCAAACCACTGAC		
2170	2190	2210
CCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCGACGGCTGCTGAAAGAGGCTG		
2230	2250	2270
TCCACCTGGCGAAACCACCGGAGCCCGAGGTTTGGGGGCTCCGCCCTGGGCTGGTTTCC		

FIG. 7B

```
      2290      2310      2330
GTCTCCTCCAGTGGAGGGAGAGGTGGGGCCCTGCTGGGGTAGAGCTGGGGACGCCACGT
      2350      2370      2390
GCCATTCCCATGGGCCAGTGAGGGCCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCC
      2410      2430      2450
AGAGTCCTGAGGAGGAGCGCCAGTTGCCCTCGCTCACAGACCACACACCCAGCCCTCCT
      2470      2490      2510
GGGTCCAGCCCAGAGGGCCCTTCAGACCCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCT
      2530      2550      2570
CAGCAGGACAGGCCCCGGGCACTGCCTTCAAGCCAAGGCTGGACTGGGTGGCTGCAGTG
      2590      2610      2630
TGGTGTTTAGTGGATAACCACATCGGAAGTGATTTTCTAAATTGGATTGAAAAAAAAA
```

FIG.7C

```

1  MLGTSGHLVWLSQGFSL.....AGRPGSSWPVD..... 29
   :.:. :.:. |. |:.|          |. |||.:. :
1  .MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQT 49

30 AVLACGWC.PGLHV.....PPLSPSSW 50
   | :. |:.| || |.          ..|||.:.|:
50 AQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSR 99

51 TPAMGLRASRNCsrTENAVCGCSPGHFCIVQGDGHCAACRAYATSSPGQR 100
   ... :. ....|.|.:.| :|.|.|| :| :.:. | | :. :.:.||
100 CSSDQV.ETQACTREQNRICrCPGWYCALSKQEGCRLCAPLRKCRPGFG 148

101 VQKGGTESQDTLCQNCPRGPSLPMGPWRNVSTRPSK..... 136
   |:.:.|||. |.:.|. |:.|. ... :.:. ..
149 VARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDA 198

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FIG.8

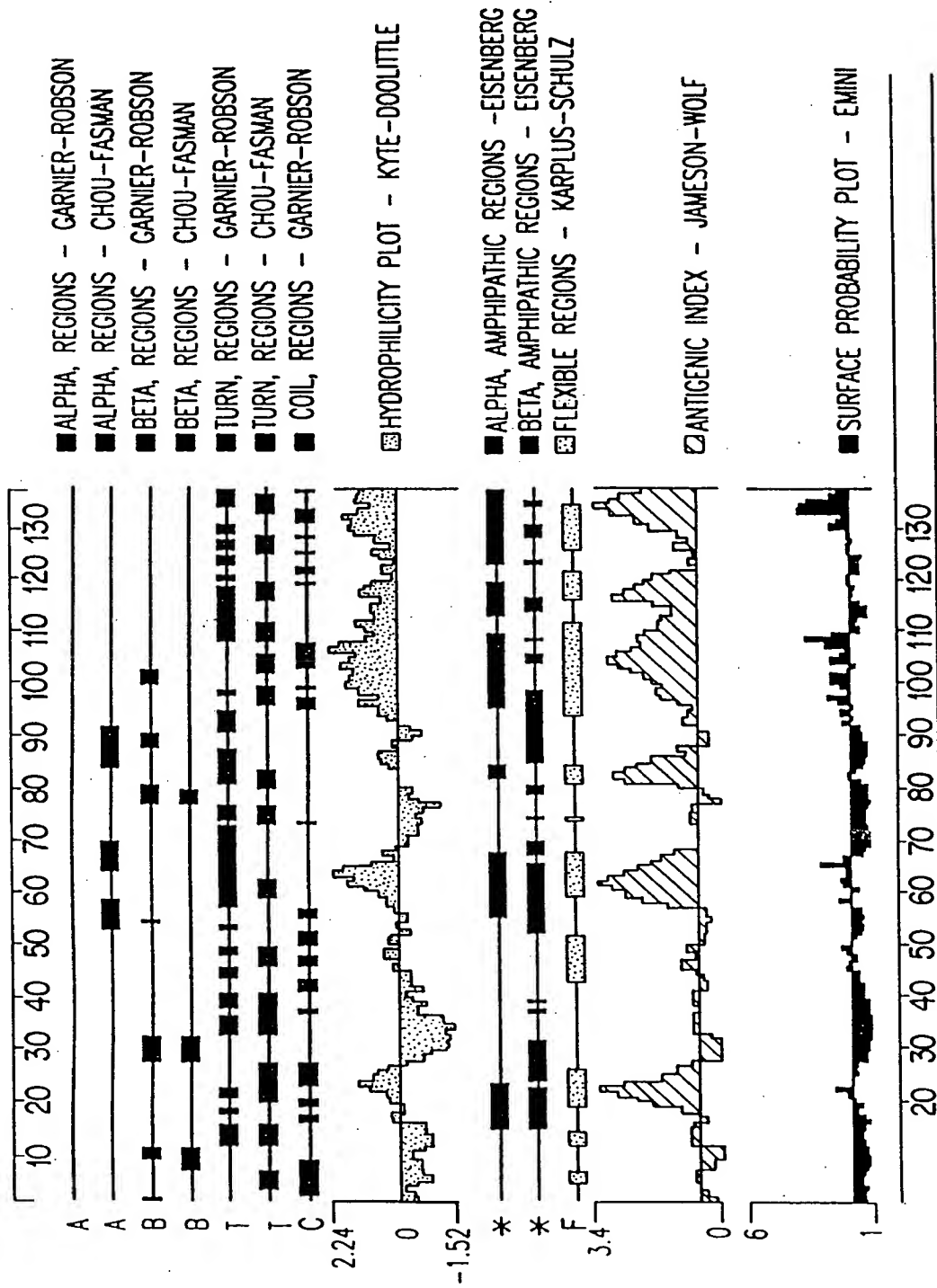


FIG.9

```

1  MEPPGDWGPPPWRSTPKTDVLRVLVLTFLGAPCYAPALPSCKEDEYPVG 50
   |||||||||||||||:||||||||||||||||||||||||||||||
1  MEPPGDWGPPPWRSTPRTDVLRVLVLTFLGAPCYAPALPSCKEDEYPVG 50

51  SECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCD 100

101 PAMGLRAS.RNCSRTENAVCGCSPGHFCIVQGDHCAACRAYATSSPGQR 149
    |.:| ... |. :: |: :|:: .. :... :|... |:..
101 PDIGSPCDLRGRGHLEAG.....AHLSPGRQKGEPDEVAFESLSAEPV 144

150 VQKGGTESQDTLCQNCPPGTFSNGTLEECQHQTCSWLVTKAGAGTSSS 199
    .|. . . . : :: :...|. |.:|:.....
145 HAANGSVPLEPHARLSMASAPCGQAGLH.....LRDRADGTPGGR 184

200 HWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVSVQRKRQEA 249

```

FIG.10

```

1  MEPPGDWGPPPWRSTPKTDVLRVLVLTFLGAPCYAPALPSCKEDEYPVG 50
   . . . . .:| :.: | |. | :||:
1  .....MLGTSGHLVWLSQGFSLAGRPGSSP.....WPVD 29

51 SECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCD 100
   . . . :||:| .|. |:..
30 AVLACGWCPGLHV.....PPLSPSSW.....T 51

101 PAMGLRASRNCSRTENAVCGCSPGHFCIVQGDHCAACRAYATSSPGQRV 150
   |||||||||||||||
52 PAMGLRASRNCSRTENAVCGCSPGHFCIVQGDHCAACRAYATSSPGQRV 101

151 QKGGTESQDTLCQNCPPGTFSNGTLEECQHQTCSWLVTKAGAGTSSSH 200
   |||||||||||||||.|. | |.: :. |.:|
102 QKGGTESQDTLCQNCPRGPSLPMGPWRNV..STRPSK..... 136

```

FIG.11

1 MEPPGDWGPPPWSTPRTDVLRLVLYLTFLGAPCYAP.....ALPSCK 43
:| :| |. | |..|
 1MLGTSGHLVWLSQGFSLAGRPGSSPWPVDAVLACGWCP 38
 44 EDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKC 93
 :. |. |:: ... |. |.. |: ...||::|. :| ::: ..|
 39 GLHVPPLSPSSWTPAMGLRASRNC SRTENAVCGCSPGHFCI..VQGDHC 86
 94 LQCQMCDPDIGSPCDLRGRGHLEAGAHLSRGRQKGE PDPEVAFESLSAEP 143
 .|. :.. :||: :| |... |... :|.. | ::: :|. |
 87 AACRAYAT..SSPGQRVQKGGTESQDTLCQNCPRGPSLPMGPWRNVSTRP 134
 144 VHAANGSVPLEPHARLSMASAPCGQAGLHLRDRADGTPGGRA. 185
 |
 135 SK..... 136

FIG.12

1GCACGAGCTGCCTCCCGCAGGCGCCACCTGTGTCCCCAGCG 42
 || ||||||| ||| ||||||| |||||||
101 TTGCCTGGACAGCTCCTGCCTCAGGCA.GCGCCACCTGTGTGCGCCAGCG 149

43 CCGCTCCACCCAGCAGGCCTGAGCCCCTCTCTGCTGCCAGACACCCCCTG 92
 ||||||| ||||||| ||||||| |||||||
150 CCGCTCCACCCAGCAGGCCTGAGCCCCTCTCTGCTGCCAGACACCCCCTG 199

93 CTGCCCCACT.CTCCTGCTGCTCGGGTCTGAGGCACAGCTTGTACACCG 141
 ||||||| ||||||| ||||||| |||||||
200 CTGCCCCACTACTCCTGCTGCTCGGGTCTGAGGCACAGCTTGTACACCG 249

142 AGGCGGATTCTCTTTCTCTTTCTCTTTCTCTTCTGGCCCACAGCCGCAGC 191
 ||||||| ||||||| ||||||| |||||||
250 AGGCGGATTCTCTTTCTCTTTCTCTTTCTCTTCTGGCCCACAGCCGCAGC 299

192 AATGGCGCTGAGTTCCTCTGCTGGAGTTCATCCTGCTAGCTGGGTCCCCG 241
 ||||||| ||||||| ||||||| |||||||
300 AATGGCGCTGAGTTCCTCTGCTGGAGTTCATCCTGCTAGCTGGGTCCCCG 349

242 AGCTGCCGGTCTGAGCCTGAGGCATGGAGCCTCCTGGAGACTGGGGGCCT 291
 ||||||| ||||||| ||||||| |||||||
350 AGCTGCCGGTCTGAGCCTGAGTCATGGAGCCTCCTGGAGACTGGGGGCCT 399

292 CCTCCCTGGAGATCCACCCCCAAAACCGACGTCTTGAGGCTGGTGCTGTA 341
 ||||||| ||||||| ||||||| |||||||
400 CCTCCCTGGAGATCCACCCCCAGAACCGACGTCTTGAGGCTGGTGCTGTA 449

342 TCTCACCTTCCTGGGAGCCCCCTGCTACGCCCCAGCTCTGCCGTCTGCA 391
 ||||||| ||||||| ||||||| |||||||
450 TCTCACCTTCCTGGGAGCCCCCTGCTACGCCCCAGCTCTGCCGTCTGCA 499

392 AGGAGGACGAGTACCCAGTGGGCTCCGAGTGCTGCCCCAAGTGCAGTCCA 441
 ||||||| ||||||| ||||||| |||||||
500 AGGAGGACGAGTACCCAGTGGGCTCCGAGTGCTGCCCCAAGTGCAGTCCA 549

442 GGTTATCGTGTGAAGGAGGCCTGCGGGGAGCTGACGGGCACAGTGTGTGA 491
 ||||||| ||||||| ||||||| |||||||
550 GGTTATCGTGTGAAGGAGGCCTGCGGGGAGCTGACGGGCACAGTGTGTGA 599

FIG. 13A

```

492 ACCCTGCCCTCCAGGCACCTACATTGCCACCTCAATGGCCTAAGCAAGT 541
      |||||||||||||||||||||||||||||||||||||||||||||||
600 ACCCTGCCCTCCAGGCACCTACATTGCCACCTCAATGGCCTAAGCAAGT 649

542 GTCTGCAGTGCCAAATGTGTGAC..... 564
      ||||||||||||||||||
650 GTCTGCAGTGCCAAATGTGTGACCCAGATATTGGTTCCCCCTGTGACCTC 699

565 .....CCAGCCATGGGCCTGCGCGCGAGCCGGAAGTGTCTC 599
      |||||||||||||||||||||||||||||||||||||||||||
1600 CCCTCCTCTTGGACTCCAGCCATGGGCCTGCGCGCGAGCCGGAAGTGTCTC 1649

600 CAGGACAGAGAACGCCGTGTGTGGTTGCAGCCCAGGCCACTTCTGCATCG 649
      ||||||||||||||||||||||||| |||||||||||||||||||||||
1650 CAGGACAGAGAACGCCGTGTGTGGCTGCAGCCCAGGCCACTTCTGCATCG 1699

650 TCCAGGACGGGGACCACTGCGCCGCGTGCCGCGCTTACGCCACCTCCAGC 699
      |||||||||||||||||||||||||||||||||||||||||||||||
1700 TCCAGGACGGGGACCACTGCGCCGCGTGCCGCGCTTACGCCACCTCCAGC 1749

700 CCGGGCCAGAGGGTGCAGAAGGGAGGCACCGAGAGTCAGGACACCCTGTG 749
      |||||||||||||||||||||||||||||||||||||||||||||||
1750 CCGGGCCAGAGGGTGCAGAAGGGAGGCACCGAGAGTCAGGACACCCTGTG 1799

750 TCAGAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCCTGGAGGAAT 799
      |||||||||||||||||||||||||||||||||||||||||||||||
1800 TCAGAACTGCCCCCGGGGACCTTCTCTCCCAATGGGACCCTGGAGGAAT 1849

800 GTCAGCACCAGACCAAGTG..... 818
      ||||||||||||||||| ||
1850 GTCAGCACCAGACCAATTGGCCTAATCATATGTGTGAAAAGAAGAAAGCC 1899

819 CAGCTGGCTGGTGACGAAGGCCGGAGCTGGG.....ACCAGCAGCTC 860
      || | | | ||| ||| | | ||| |
1900 AAGGGGTGAGCACACGGTGGCCCCATCAGGGTTCATGTCCCAGCCGTCA 1949

861 CCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTTT 910
      || || || | | | | | | | | | | |
1950 CCTCTTGGAGCTCTGTACCCCAAGCCTGGGAGGTGGCCCCAGAGCTTTT 1999

```

FIG. 13B

911	GCTCCACAGTTGGCCTAATCATATGTGTGAAAAGAAGAAAGCCAAGGGGT	960
2000	CCAGGATCCGCGGCTCCTCCCAGGGCAGCCACTGCAGGCTGGGGCAGGTG	2049
961	GATGTAGTCAAGGTGATCGTCTCCGTCCAGCGG.AAAAGACAGGAGGCAG	1009
2050	TATGTAGTCAAGGTGATCGTCTCCGTCCAGCGGTAAAAGACAGGAGGCAG	2099
1010	AAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCTCCGGACGTCACC	1059
2100	AAGGTGAGGCCACAGTCATTGA.GCCCTGCAGGCCCTCCGGACGTCACC	2148
1060	ACGGTGGCCGTGGAGGAGACAATACCCTCATTACGCGGGAGGAGCCCAA	1109
2149	ACGGTGGCCGTGGAGGAGACAATACCCTCATTACGCGGGAGGAGCCCAA	2198
1110	CCACTGACCCACAGACTCTGCACCCGACGCCAGAGATACCTGGAGCGAC	1159
2199	CCACTGACCCACAGACTCTGCACCCGACGCCAGAGATACCTGGAGAGAC	2248
1160	GGCTGAATGAAAGAGGCTGTCCACCTGGCGGAACCACCGGAGCCCGGAGG	1209
2249	GGCTG.CTGATAGAGGCTGTCCACCTGGCGAAACCACCGGAGCCCGGAGG	2297
1210	CTTGGGGGCTCCACCCTGGACTGGCTTCCGTCTCCTCCAGTGGAGGGAGA	1259
2298	CTTGGGGGCTCCGCCCTGGGCTGGTTTCCGTCTCCTCCAGTGGAGGGAGA	2347
1260	GGTGGCGCCCCTGCTGG.GGTAGAGCTGGGGACGCCACGTGCCATTCCCA	1308
2348	GGTGGTGCCCCTGCTGGTGGTAGAGCTGGGGACGCCACGTGCCATTCCCA	2397
1309	TGGGCCAGTGAGGGCCTGG.GGCCTCTGTTCTGCTGTGGCCTGAGCTCCC	1357
2398	TGGTTCAGTGAGGGGCTGGTGGCCTCTGTTCTGCTGTGGCCTGAGCTCCC	2447
1358	CAGAGTCCTGAGGAGGAGCGCCAGTTGCCCTCGCTCACAGACCACACAC	1407
2448	CAGAGTCCTGAGGAGGAGCCCCAGTTGCCCTCGCTCACAGACCACACAC	2497

FIG.13C

1408	CCAGCCCTCCTGGGCCAACCCAGAGG . GCCTTCAGACCCCAGCTGTGTGC	1456
2498	CCAGCCCTCCTGGGCCAACCCAGAGGCCCTTCAGACCCCAGCTGTCTGC	2547
1457	GCGTCTGACTCTTGTGGCCTCAGCAGGACAGGCCCCGGGCACTGCCTCAC	1506
2548	GCGTCTGACTCTTGTGGCCTCAGCAGGACAGGCCCCGGGCACTGCCTCAC	2597
1507	AGCCAAGGCTGGACTGGGTTGGCTGCAGTGTGGTGTGTTAGTGGATACCAC	1556
2598	AGCCAAGGCTGGAATGGGTTGGCTGCAGTGTGGTGTGTTAGTGGATACCAC	2647
1557	ATCGGAAGTGATTTTCT . . AAATTGGATTTGAATTCGGCTCCTGTTTTCT	1604
2648	ATCGGAAGTGATTTTCTAAAAATTGGATTTGAATTCGGAAAAAA	2692

FIG. 13D

1GCACGAGCTGCCTCCCGCAGGCGC 24
 | | | | |
 701 GTTGCTTCCCTGGGAGATGACCGTCTTCTCCAGCAGAAAGGTTGAAGGTC 750
 25 CACCTGTGTCCCCAGCGCCGCTCCACCCAGCAGGCCTGAGCCCCTCTCT 74
 | | | | | | | | | | | | | |
 751 CCACCCTGAGCGGCACCCTGGTCACATGCCTGCGTCCAGGAGAGCTGCAG 800
 75 GCTGCCAGACACCCCCTGCTGCCCACTCTCCTGCTGCTCGGGTTCTGAGG 124
 | | | | | | | | | | | | | |
 801 GGTGAAGCCTGTGTGCCCCAGATAACCCCTTCCATGGGCCAGACAAAGC 850
 125 CACAGCTTGTACACCGAGGCGGATTCTCTTTCTTTCTTTCTTTCTCTTC 174
 | | | | | | | | | | | | | |
 851 CTCATCAGATCTGAGCTTCTGAGGCTCAGGATGGGCCTTCCCAGAAGC 900
 175 TGGCCACACA.....GCCGCAGCAATGGCGCTGAGTTCCTCTGCTGGAGTT 219
 | | | | | | | | | | | | | |
 901 AGGCCCAGAGGGAGGCTGCCTCCAGATCCCCTGTCCCCTGGGGCTGTGGG 950
 220 CATCCTGCTAGCTGGGTTCCCGAGCTGCCGGTCTGAGCCTGAGGCATGGA 269
 | | | | | | | | | | | | | |
 951 TGTCCCTGAATGTCAGGGCCATGGGAGGGCCCTGGGCTTCAGGGGTTGG 1000
 270 GCCTCCTGGAGACTGGGGGCCTCCTCC.....CTGGAGATCCACCCCCAA 314
 | | | | | | | | | | | | | |
 1001 GGAAAGTGAACACTCTGCTCTTTGTCCACCTTCGGGAGGACAACCTTCAA 1050
 315 A.....ACCGACGTCTTGAGGCTGGTGCTGTATCTCACCTTCCTGGGA 357
 | | | | | | | | | | | | | |
 1051 ATGCTGACCCTGGGCCCTAACTGACCTGAGACTTCAGAGCTTCTTGGGA 1100
 358 GCCCCCTGCTACGCCCCAGCTCTGCCGTCTGCAAGGAGGACGAGTACCC 407
 | | | | | | | | | | | | | |
 1101 GGAGCTGGGGTCCCCAGCGGAGCCTGGGATGGAGCAGGGATGGCTGCCC 1150
 408 AGTGGGCTCCGAGTGCTGCCCAAGTGCAGTCCAGGTTATCGTGTGAAGG 457
 | | | | | | | | | | | | | |
 1151 CAGGGAGGGGGCGGTGGGGCCTTCCATCCTGCTCTGCCCTCCTCGTCCTC 1200

FIG. 14A

```

458  AGG..CCTGCGGGGAGCTGACGGGCACAGTGTGTGAACCCTGCCCTCCAG 505
      ||  ||  ||  |  |||  |  |  |  |  |  |  |  |  |  |  |
1201  TGGCCCCAGCTCAGTCCTGTCCATCTCCAGCTCTAACCATTGTGGCCCG 1250

506  GCACCTACATTGCCACCTCAATGGCCTAAGCAAGTGTCTGCAGTGCC.. 553
      |||  |  |  ||  |  |  |  |  |  |  |  |  |  |||  |  ||
1251  ACACTGGCTCTCCCTCTACCTTCTGTCCTTGTCTGACACTGGTCTCCCGT 1300

554  .AAATGTGTGACCCAGCCATGGGCCTGCGCGGAGCCGGAAGTGTCCAG 602
      ||  |  |  |  |  |  |  |||  |  |  |  |  |||
1301  GCTCTGGGGTCTCTGCACTGATGGCTGCCTCCCGCTTCTCTCCCTCTCC 1350

603  GACAGAGAACGCCGTGTGTGGTTGCAGCCCAGGCCACTTCTGCATCGTCC 652
      |  |  |  |  ||  |||  |  |  |  |  ||  ||  |  |
1351  CTCTGCCGTCCTGTCTCCTGTGGCCAGTCTCTCCTTGTCTTCTCTCCT 1400

653  AGGACGGGGACCACTGCGCCGCGTGCCGCGCTTACGCCACCTCCAGCCCG 702
      |  |  |  |||  |  |  |  |  |  |  |  ||  |  |
1401  CCTTCCTTCTCTCCACCTCCCATAGCCGAGCTTGGAAAAGTCAGACAGA 1450

703  GGCCAGAGGGTGCAGAAAGGAGGCACCGAGAGTCAGGACACCCTGTGTCA 752
      |  |||  ||  |||  ||  ||  |  |  |  |||  ||  |
1451  CCTCTGAGGTCTCATCCTGGAGCTGCCACCAGCCCAGCCTCCCTGGGACC 1500

753  GAACTGCCC..CCCGGGGACCTTCTCTCCAATGGGACCCTGGAGG.... 796
      ||  |  |  ||  |||  |||  ||  ||  ||  |||
1501  TGTCTTCACTGCCTGGGGCCCTGGGAGCCAGGGAGGCTCCCTGAGGCTGA 1550

797  .....AATGTCAGCACCAG 810
      |  |  |||
1551  GTGAACACTGGGCGCTGCACCTGCCTCTCCACGTCCTCGGCCCACTCC 1600

811  ACCAAGTGCAGCTGGCTGGTGACGAAGGCCGGAGCTGGGACCAGCAGCTC 860
      ||  |||||||||||||||||||||||||||||||||||||||
1601  CGCAGGTGCAGCTGGCTGGTGACGAAGCCCGGAGCTGGGACCAGCAGCTC 1650

861  CCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTTT 910
      |||||||||||||||||||||||||||||||||||||||
1651  CCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTTT 1700

```

FIG.14B

```

911  GCTCCACAGTTGGCCTAATCATATGTGTGAAAAGAAGAAAGCCAAGGGGT 960
      |||
1701 GCTCCACAGTTGGCCTAATCATATGTGTGAAAAGAAGAAAGCCAAGGGGT 1750
      |||
961  GATGTAGTCAAGGTGATCGTCTCCGTCCAG..... 990
      |||
1751 GATGTAGTCAAGGTGATCGTCTCCGTCCAGGTATTGATCCTCCTCCCCCT 1800
      |||
991  .....CGGAAAAGACAGGAGGCA 1008
      |||
2001 GGCAGGGTCTCCACGATTCGTGTGCTCACAGCGGGAAAAGACAGGAGGCA 2050
      |||
1009 GAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCTCCGGACGTCAC 1058
      |||
2051 GAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCTCCGGACGTCAC 2100
      |||
1059 CACGGTGGCCGTGGAGGAGACAATACCCTCATTAC.GGGGAGGAGCCCA 1107
      |||
2101 CACGGTGGCCGTGGAGGAGACAATACCCTCATTACGGGGGAGGAGCCCA 2150
      |||
1108 AACCACTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCG 1157
      |||
2151 AACCACTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCG 2200
      |||
1158 ACGGCTGAATGAAAGAGGCTGTCCACCTGGCGGAACCACCGGAGCCCGGA 1207
      |||
2201 ACGGCTG.CTGAAAGAGGCTGTCCACCTGGCGAAACCACCGGAGCCCGGA 2249
      |||
1208 GGCTTGGGGGCTCCACCCTGGACTGGCTTCCGTCTCCACAGTGGAGGGA 1257
      |||
2250 GGTGGGGGCTCCGCCCTGGGCTGGTTCCGTCTCCTCCAGTGGAGGGA 2299
      |||
1258 GAGGTGGCGCCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCC 1307
      |||
2300 GAGGTGGGGCCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCC 2349
      |||
1308 ATGGGCCAGTGAGGGCCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCC 1357
      |||
2350 ATGGGCCAGTGAGGGCCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCC 2399
      |||

```

FIG. 14C

1358	CAGAGTCCTGAGGAGGAGCGCCAGTTGCCCTCGCTCACAGACCACACAC	1407
2400	CAGAGTCCTGAGGAGGAGCGCCAGTTGCCCTCGCTCACAGACCACACAC	2449
1408	CCAGCCCTCCTGGG.CCAACCCAGAGGG.CCTTCAGACCCCAGCTGTGTG	1455
2450	CCAGCCCTCCTGGGTCCAGCCCAGAGGGCCCTTCAGACCCCAGCTGTCTG	2499
1456	CGCGTCTGACTCTTGTGGCCTCAGCAGGACAGGCCCCGGGCACTGCCTCA	1505
2500	CGCGTCTGACTCTTGTGGCCTCAGCAGGACAGGCCCCGGGCACTGCCTTC	2549
1506	CAGCCAAGGCTGGACTGGGTTGGCTGCAGTGTGGTGTTTAGTGGATACCA	1555
2550	AAGCCAAGGCTGGACTGGGTTGGCTGCAGTGTGGTGTTTAGTGGATACCA	2599
1556	CATCGGAAGTGATTTTCTAAATTGGATTGAATTCGGCTCCTGTTTTCTA	1605
2600	CATCGGAAGTGATTTTCTAAATTGGATTGAAAAAAAAA.....	2637

FIG. 14D


```

1  CCCCTTCTACAGGAAACCCGGAGTGGACTGGAACGGTGCAGGGGAGAA  50
    ||  |  ||||  |||  |  |||  |  |||  |
1  ...AAAGCTCGGGCTCCACCGGGGACGACCGCTCCTAGAAACTGAGTGGT  47

51  CTCGCCCTCCCATCGGGCGCCTCCTTCATACCGGCCCTTCCCCTCGGCT  100
    || |||  ||  ||  ||  |||  |  |||  |  ||||  ||
48  ATCCCCCGGGCCTGCAGG.AATTCCAACCTGCCTGAAGGGACCCTGCCCT  96

101  TTGCCTGGACAGCTCCTGCCTCAGGCAGCGCCACCTGTGTGCCCAGCGC  150
     |||  |  ||  |||  |  |  |||  ||  ||
97  GGAAGTG..ACAGTGCAAGCTCGGCGTCCTGCCCATCTGGGAAGAAGGCT  144

151  CGCTCCACCCAGCAGGCCTGAGCCCCTCTCTGCTGCCAGACACCCCCTGC  200
    |||  ||||  ||  |  |||  |||  ||  |||  ||
145  GGTTCCTCCCATCAACGAAGCCCTCCAGGACCTTCCTGCAAGCCCTCGT  194

201  TGCCCACTACTCCTGCTGCTCGGGTTCTGAGGCACAGCTTGTACACCGA  250
    |||  |  ||  |  ||  |  ||  |  |||  |
195  CCCACACGCAGCTCTGCCGTCCCTTGGTGTCCCTCCCGGCCTCA...GGT  241

251  GGCGGATTCTCTTTCTCTTTCTCTTTCTCTTCTGGCCCA.CAGCCGCAGC  299
     ||  ||  |  ||  |  |||  ||||  ||  |  |
242  CCTCCATGCTGGGTACCTCTGGGCACCTCGTTTGGCTGAGCCAGGGGTTC  291

300  AATGGCGCTGAGTTCCTCTGCTGGAGTTCATCCTGCTAGCTGGGTTCCCG  349
    |  |||  ||  ||  ||  |||  ||  |  ||  ||
292  AGCCTGGCAGGGCGCCCTGGCAGCAGTCCTTGGCCTGTGGATGCTGTCCT  341

350  AGCTGCCGTCTGAGCCTGAGTCATGGAGCCTCCTGGAGACTGGGGGCCT  399
    ||  ||  ||  ||  |  ||  ||  ||  ||  ||
342  GGCCTGTGGATGGTGTG.....CCGGCCTCCACGTACCCCCTCTCAGCCC  386

400  CCTCCCTGGAGATCCACCCCAGAACCGACGTCTTGAGGCTGGTGCTGTA  449
    |  |||  |  ||||  ||  |  |  |  |  ||||  |
387  CTCCTCTTGGACTCCAGCCATGGGCCTGCGCGGAGCCGGAAGTGTCCA  436

450  TCTCACCTTCCTGGGAGCCCCCTGCTACGCCCAGCTCTGCCG.TCCTGC  498
     ||  |  ||  |  |  |  ||  ||  ||  ||  |  |
437  GGACAGAGAACGCCGTGTGTGGCTGCAGCCAGGCCACTTCTGCATCGTC  486

```

FIG.15A

499 AAGGAGGACGAGTACCCAGTGGGCTCCGAGTGCTGCCCCAAGTGCAGTCC 548
 |||| | || || | | | | | | |||| |
 487 CAGGACGGGGACCACTGCGCCGCGTGCCGCGCTTACGCCACCTCCAGCCC 536
 549 AGGTTATCGTGTGAAGGAGGCCTGCGGGGAGCTGACGGGCACAGTGTGTG 598
 || | | ||| || ||| || ||| || ||| |||||
 537 GGGCCAGAGGGTGCAGAAGGGAGGCACCGAGAGTCAGGACACCCTGTGTC 586
 599 AACCTGCCCTCCAGGCACCTACATTGCCACCTCAATGGCCTAAGCAAG 648
 | ||||| | || | | | |||| | | | |
 587 AGAACTGCCCCCGGGGACCTT..CTCTCCAATGGGACCCTGGAGGAATG 634
 649 TGTCTGCAGTGCCAAATGTGTGACCCAGATATTGGTTCCCCCTGTGACCT 698
 | | | |||| | |||| || | || | ||||| |||
 635 TCAGCACCAGACCAAGTAAGTGAACCCGGGGGAGGCCAGCTCTGTGCCCT 684
 699 CAGGGGAAGAGGTCACCTGGAGGCTGGTGCCACCTGAGTCCAGGCAGAC 748
 || | | ||| | | | | | ||| | |
 685 GGGGAGGGGGCTCCACGTTGCTTCCCTGGGAGATGACCGTCTTCTCCAGC 734
 749 AGAAAGG.....GGAACCAGACCCAGAGGTGGCCTTTGAGTCACTGAGCG 793
 ||||| || ||| | || || ||| |||
 735 AGAAAGGTTGAAGGTCCACCCCTGAGCGGCACCCTGGTCACATGCCTGCG 784
 794 CAGAGCCTGTCCATGCGGCCAACGGCTCTGTCCCCTTGGAGCCTCATGCC 843
 || | || || ||| || | ||| |||
 785 TCCAGGAGAGCTGCAGGGTGAAGCCTGTGTGCCCCAGATAACCCCTTCCA 834
 844 AGGCTCAGCATGGCCAGTGCTCCCTGCGGCCAGGCAGGACTGCACCTGCG 893
 || | | || || | | | | | ||| |
 835 TGGGCCCAGACAAAGCCTCATCAGATCTGAGCTTCCTGGAGGCTCAGGAT 884
 894 GGACAGGGCTGACGGCACACCTGGGGGCAGGGCCTGAGCCTACAGGGAGG 943
 || | | || || || ||| || | |
 885 GGGCCTTCCCAGAAGCAGGCCAGAGGGAGGCTGCCTCCAGATCCCCTGT 934
 944 CACAGGGCAGGTGGGCTAGCCATGAACAGAAGAGGAAGCTGGAGTGCTTT 993
 | | || || | || |||| || | | | | |
 935 CCCCTGGGGCTGTGGGTGTCCCTGAATGTCAGGGCCATGGGAGGGCCCCT 984

FIG.15B

994 GGGGGTTCATGCATGTAGGCTGGGATTTGGGGCTCACACCTCAACCTGCA 1043
 ||| | | | | | | | | | | | | |
 985 GGGCTTCAGGGGTTGGGGAAGTGAACACTCTGCTCTTTGTCCACCTTCG 1034
 1044 TGCCCAGTTCCATGCCCCTCCCCTCTTGTGAAAGCACCTGTCTACTTGGG 1093
 | | | | | | | | | | | | | | | |
 1035 GGAGGACAACCTTCAAATGCTGACCCTGGGCCCTAACT.....GA 1075
 1094 CTGAGGATGTGGGGGCACAGGTGGCAGGTGAGGCTGCCCTCAGGAGGGGC 1143
 | | | | | | | | | | | | | | | | | |
 1076 CCTGAGACTTCAGAGCTTCTTGGGAGGAGCTGGGGTCCCCCAGCGGAGCC 1125
 1144 CCAGGCCCAGCTTGTACCCACCTCCACCAGTACCTGAAGAAGTGGGGCT 1193
 | | | | | | | | | | | | | | | | | |
 1126 TGGGATGGAGCAGGGATGGCTGCCCA.....GGGAGGGGGCGGTGG 1167
 1194 CTCACCCTACCTGCCTCTGCCATTGGAATGGCCTGGTTTGCACAGATGGG 1243
 | | | | | | | | | | | | | | | | | |
 1168 GGCCTTCCATCCTGCTCTGCCCTCCTCGTCCTCTGGCCCCAGCTCAGTCC 1217
 1244 AAACCCGTTTGAGGGGTGGGTGTCTGGGTGGGCACGTGGGGCGAGGACCT 1293
 || | | | | | | | | | | | | | | | |
 1218 TGTCCATCTCCAGCTCTAACCATTTGTGGCCCGACACTGGCTCTCCCTCT 1267
 1294 GCCTGAGGGACCCTGCCCTGGAAGTACAGTGCAAGCTCGGCGTCCTGCC 1343
 ||| | | | | | | | | | | | | | | | |
 1268 ACCTTCTGTCTTGTCTGACACTGGTCTCCCGTGCTCTGGGGTCTCTGCA 1317
 1344 CATCTGGGCAGAAGGCTGGTTTCTCCCATCAACGAAGCCCTCCAGGACC 1393
 | ||| | | | | | | | | | | | | | | | |
 1318 CTGATGGCTGCCTCCCGCTTCTCTCCCTCTCCCTCTGCCGTCTGTCTC 1367
 1394 TTCCTGCAAGCCCTCGTCCCACACGCAGCTCTGCCGTCCCTTGGTGTCCC 1443
 | ||| | | | | | | | | | | | | | | | |
 1368 CTGTGGCCAGTCTCTCCTTGTCTCTTCTCCTCCTTCTCTCTCCACC 1417
 1444 TCCCGGCCTCAGGTCCTCCA....TGCTGGGTACCTCTGGGCACCTCGTT 1489
 |||| | | | | | | | | | | | | | | | |
 1418 TCCCATAGCCGAGCTTGGAAAAGTCAGACAGACCTCTGAGGTCTCATCC 1467

FIG.15C

1490 TGGCTGAGCCAGGGGTTTCAGCCTGGCAGGGCGCCCTGGCAGCAGTCCTTG 1539
 ||| |||| | ||||| | ||| | | | |
 1468 TGGAGCTGCCACCAGCCCAGCCTCCCTGGGACCTGTCTTCACTGCCTGGG 1517
 1540 GCCTGTGGATGCTGTCCTGGCCTGTG.GATGGTGTCCCGCCCTCCACGTA 1588
 ||| ||| | | | | ||| | ||| |
 1518 GCCCTGGGAGCCAGGGAGGCTCCCTGAGGCTGAGTGAACACTGGGCGCTG 1567
 1589 CCCCTCTACCCCCTCCTCTTGGA CTCCAGCCATGGGCCTGCGCGCGAGC 1638
 | ||| | ||| | ||| | ||| | ||| |
 1568 CACCTGCCTCTCCACGTCCTCGGCCCA.....CTCCCGC 1603
 1639 CGGAAGTGTCCAGGACAGAGAACGCCGTGTGTGGCTGCAGCCCAGGCCA 1688
 || | ||| | ||| ||| ||| |||| |||
 1604 AGGTGCAGCTGGCTGGTGACGAAGCCCGGAGCTGGGACCAGCAGCTCCA 1653
 1689 CTTCTGCATCGTCCAGGACGGGGACCACTGCGCCGCGTGCCGCGCTTACG 1738
 || | | | ||| | ||| |
 1654 CTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTTTGCT 1703
 1739 CCACCTCCAGCCCGGGCCAGAGGGTGCAGAAGGGAGGCACCGAGAGTCAG 1788
 |||| ||| | ||| ||| ||| | ||| |
 1704 CCACAGTTGGCCTAATCATATGTGTGAAAAGAAGAAAGCCAAGGGGTGAT 1753
 1789 GACACCCTGTGTCAGAACTGCCCCCGG...GGACCTTCTCTCCAATGG 1835
 | | | ||| ||| ||| ||| ||| |||
 1754 GTAGTCAAGGTGATCGTCTCCGTCCAGGTATTGATCCTCCTCCCCCTCTC 1803
 1836 GACCCTGGAGGAATGTCAGCACCAGACCAATTGGCCTAATCATATGTGTG 1885
 || | | |||| || | | ||||
 1804 CCTCCCCCTCCACCTTCCACCTCCCCTCTCCCCGCTGGGGCTGGTGTT 1853
 1886 AAAAGAAGAAAGCCAAGGGG...TGAGCACACGGTGGCCCCATCAGGGTT 1932
 | | | |||| || | | ||| |||
 1854 TCTGGTGTACATGGTGGGGGCTCCAGTTCTCTGAGGGTCCTGAGTCTTT 1903
 1933 CATGTCCCCAGCCGTACCTCTTGAGCTCTGTACCCCAAGCCTGGGAG 1982
 || || | || |||| | | | |||| || |
 1904 CAAGTACAGCCACGGTAGCTCAGGAA.....AGAACCACCCCCTCAA 1947

FIG.15D

FIG. 15E

2481 GCTCACAGACCACACACCCAGCCCTCCTGGG.CCAACCCAGAGGCCCCCTT 2529
|||||
2433 GCTCACAGACCACACACCCAGCCCTCCTGGGTCCAGCCCAGAGGGCCCTT 2482
2530 CAGACCCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCAGGACAGG 2579
|||||
2483 CAGACCCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCAGGACAGG 2532
2580 CCCCGGGCACTGCCTCACAGCCAAGGCTGGAATGGGTTGGCTGCAGTGTG 2629
|||||
2533 CCCCGGGCACTGCCTTCAAGCCAAGGCTGGACTGGGTTGGCTGCAGTGTG 2582
2630 GTGTTTAGTGGATACCACATCGGAAGTGATTTTCTAAAAATTGGATTTGA 2679
|||||
2583 GTGTTTAGTGGATACCACATCGGAAGTGATTTTCTAAA.....TTGG 2624
2680 ATTCGGAAAAAAA 2692
|||
2625 ATTTGAAAAAAA 2637

FIG.15F

TNFR-I	V	C	PQGYIHPQNNSI	C	C	TK	C	HKGTYLYND	C	C	PGPGQDTD	C	R
TNFR-II	T	C	RLREYYDQTAQM	C	C	SK	C	SPGQHAKVF	C	C	TKTSDTV	C	D
CD40	A	C	REKQYLINSQ	C	C	SL	C	QPGQKLVSD	C	C	TEPTETE	C	L
4-1BB	-	-	-	-	-	SN	C	PAGTF	C	C	DNNRNQI	C	S
TR-2	S	C	KEDEYPVGSE	C	C	PK	C	SPGYRVEKA	C	C	GELTGTV	C	E

TNFR-I	E	C	ESGSFTASENHLRH	C	LS	C	SK	C	RKEMGQVEISS	C	C	TVDRDTV	C	G
TNFR-II	S	C	EDSTYTQLWNWPE	C	LS	C	GSR	C	SSDQVETQA	C	C	TREQNRI	C	T
CD40	P	C	GESEFLDTWNRETH	C	HQ	C	HY	C	DPNLGLRVQKQ	C	G	TSETDTI	C	T
4-1BB	P	C	PPNSFSSAGGQRT	C	DI	C	RQ	C	KGVFRTKE	C	C	SSTSNAE	C	D
TR-2	P	C	PPGTYTAHLNGLSK	C	LQ	C	QM	C	DPAMGLRASRN	C	C	SRTENAV	C	G

TNFR-I	C	R	KNQRYRHWSENLFQ	C	FN	C	SL	C	LNGTVHLS	C	C	QEKQNTV	C	T
TNFR-II	C	R	PGWY	C	RL	C	APLRK	C	RPGFGVARP	C	G	TETSDWV	C	K
CD40	C	E	EGWH	C	ES	C	VLHRS	C	SPGFGVKQIAT	C	G	VSDTI	C	E
4-1BB	C	T	PGFH	C	SM	C	EQD	C	KQGQELTKKG	C	C	KD	C	-
TR-2	C	S	PGHF	C	AA	C	RAYAT	S	SPGQRVQKG	C	G	TESQDTL	C	Q

TNFR-I	-	C	HAGFFLRENE	C	VS	C	SN	C	KKSLE	C	C	TKL	C	L
TNFR-II	P	C	APGTFSTNTSSDI	C	RP	C	HQI	C	NWVAIP	C	G	NASMDAV	C	T
CD40	P	C	PVGFFSNVSSAFEK	C	HP	C	WTS	C	ETKDLWQQA	C	G	TNKTDWV	C	G
4-1BB	-	C	F-GTFNKQKRG I	C	RP	C	WTN	C	SLDGKSVLWN	C	G	TKERDWN	C	G
TR-2	N	C	PPGTFSPNGTLEE	C	QH	C	QTK	C	SWLVTKA	C	G	AGTSSSH	C	V

FIG.16